

CLEAN VERSION OF REPLACEMENT PARAGRAPHS IN
THE SPECIFICATION PURSUANT TO 37 C.F.R. §1.121(b)

IN THE SPECIFICATION

On page 65, please delete the paragraph beginning on line 23 and ending on page 67, line 8, and replace with the following paragraph:

In some embodiments, the software provides a scoring system to indicate the quality (e.g., the likelihood of performance) of the assay designs. In one embodiment, the scoring system includes a starting score of points (e.g., 100 points) wherein the starting score is indicative of an ideal design, and wherein design features known or suspected to have an adverse affect on assay performance are assigned penalty values. Penalty values may vary depending on assay parameters other than the sequences, including but not limited to the type of assay for which the design is intended (e.g., monoplex, multiplex) and the temperature at which the assay reaction will be performed. The following example provides an illustrative scoring criteria for use with some embodiments of the INVADER assay based on an intelligence defined by experimentation. Examples of design features that may incur score penalties include but are not limited to the following [penalty values are indicated in brackets, first number is for lower temperature assays (e.g., 62-64 °C), second is for higher temperature assays (e.g., 65-66 °C)]:

1. [100:100] 3' end of INVADER oligonucleotide resembles the probe arm:

ARM SEQUENCE:

PENALTY AWARDED IF INVADER

ENDS IN:

Arm 1: CGCGCCGAGG (SEQ ID NO:1)	5'...GAGGX or	5'...GAGGXX
Arm 2: ATGACGTGGCAGAC (SEQ ID NO:2)	5'...CAGACX or	5'...CAGACXX
Arm 3: ACGGACGCGGAG (SEQ ID NO:3)	5'...GGAGX or	5'...GGAGXX
Arm 4: TCCGCGCGTCC (SEQ ID NO:4)	5'...GTCCX or	5'...GTCCXX

2. [70:70] a probe has 5-base stretch (i.e., 5 of the same base in a row) containing the polymorphism;

3. [60:60] a probe has 5-base stretch adjacent to the polymorphism;

4. [50:50] a probe has 5-base stretch one base from the polymorphism;

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5. [40:40] a probe has 5-base stretch two bases from the polymorphism;
 6. [50:50] probe 5-base stretch is of Gs - additional penalty;
 7. [100:100] a probe has 6-base stretch anywhere;
 8. [90:90] a two or three base sequence repeats at least four times;
 9. [100:100] a degenerate base occurs in a probe;
 10. [60:90] probe hybridizing region is short (13 bases or less for designs 65-67°C; 12 bases or less for designs 62-64°C)
 11. [40:90] probe hybridizing region is long (29 bases or more for designs 65-67°C, 28 bases or more for designs 62-64°C)
 12. [5:5] probe hybridizing region length - per base additional penalty
 13. [80:80] Ins/Del design with poor discrimination in first 3 bases after probe arm
 14. [100:100] calculated INVADER oligonucleotide Tm within 7.5°C of probe target Tm (designs 65-67°C with INVADER oligonucleotide less than < 70.5°C, designs 62-64°C with INVADER oligonucleotide < 69.5°C)
 15. [20:20] calculated probes Tms differ by more than 2.0°C
 16. [100:100] a probe has calculated Tm 2°C less than its target Tm
 17. [10:10] target of one strand 8 bases longer than that of other strand
 18. [30:30] INVADER oligonucleotide has 6-base stretch anywhere - initial penalty
 19. [70:70] INVADER oligonucleotide 6-base stretch is of Gs - additional penalty
 20. [15:15] probe hybridizing region is 14, 15 or 24-28 bases long (65-67°C) or 13,14 or 26,27 bases long (62-64°C)
 21. [15:15] a probe has a 4-base stretch of Gs containing the polymorphism

Please insert the attached Sequence Listing as new pages --118-119--.

IN THE CLAIMS

Please renumber the Claims pages from pages "118-127" to --120-129--.